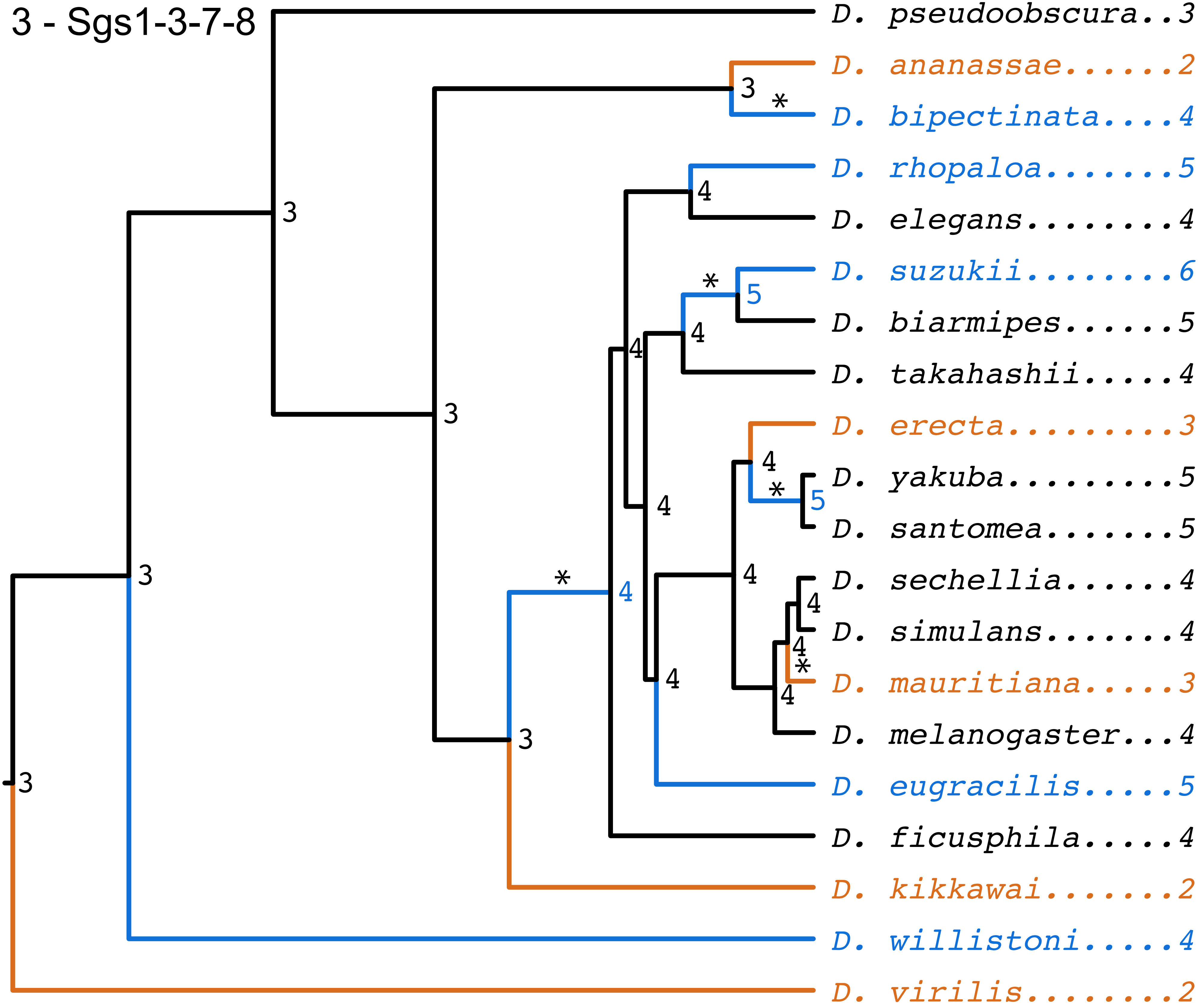
3 - Sgs1-3-7-8
D. pseudoobscura..3
D. ananassae......2
D. bipectinata....4
D. rhopaloa.......5
D. elegans........4
D. suzukii........6
D. biarmipes......5
D. takahashii.....4
D. erecta.........3
D. yakuba.........5
D. santomea.......5
D. sechellia......4
D. simulans.......4
D. mauritiana.....3
D. melanogaster...4
D. eugracilis.....5
D. ficusphila.....4
D. kikkawai.......2
D. willistoni.....4
D. virilis........2
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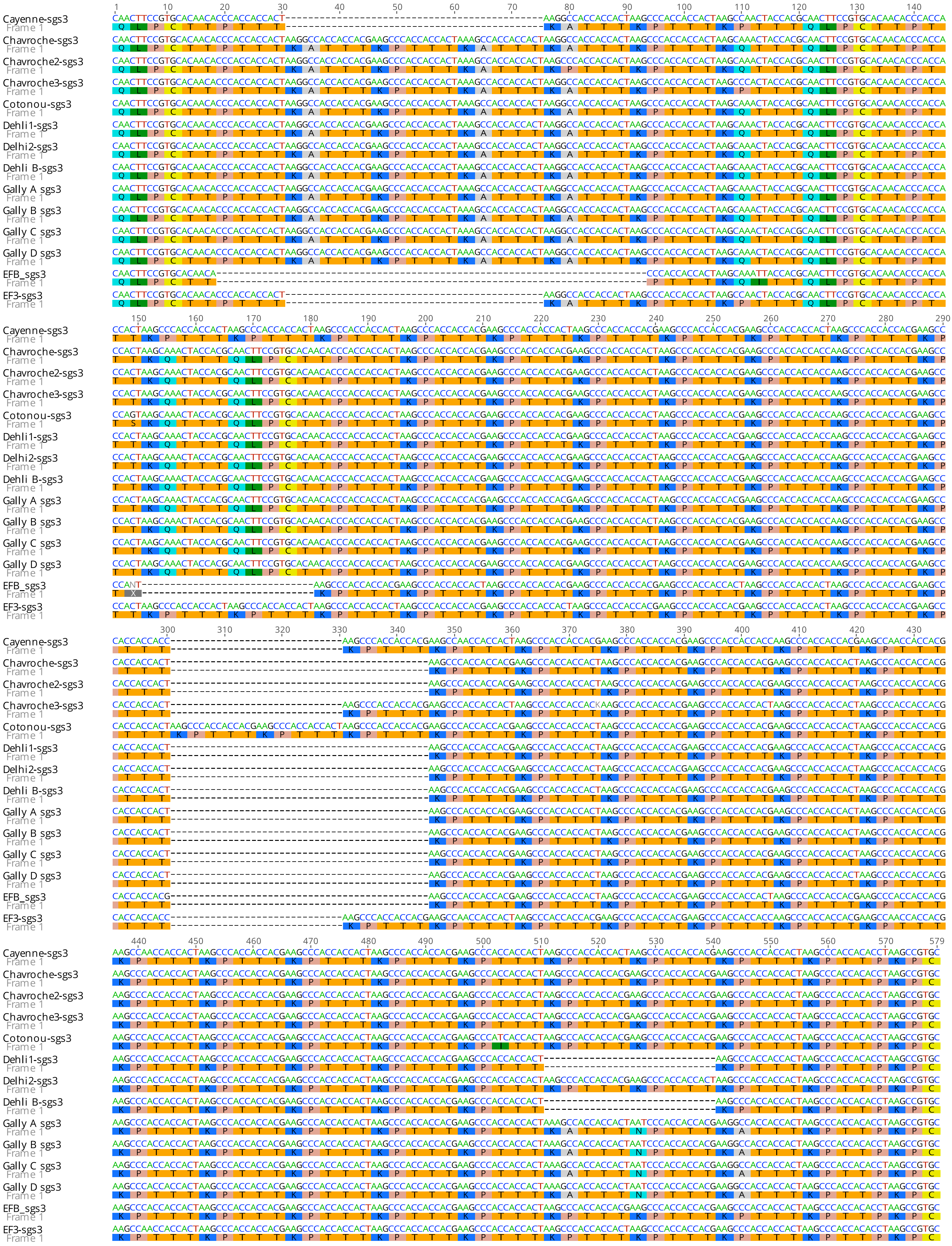
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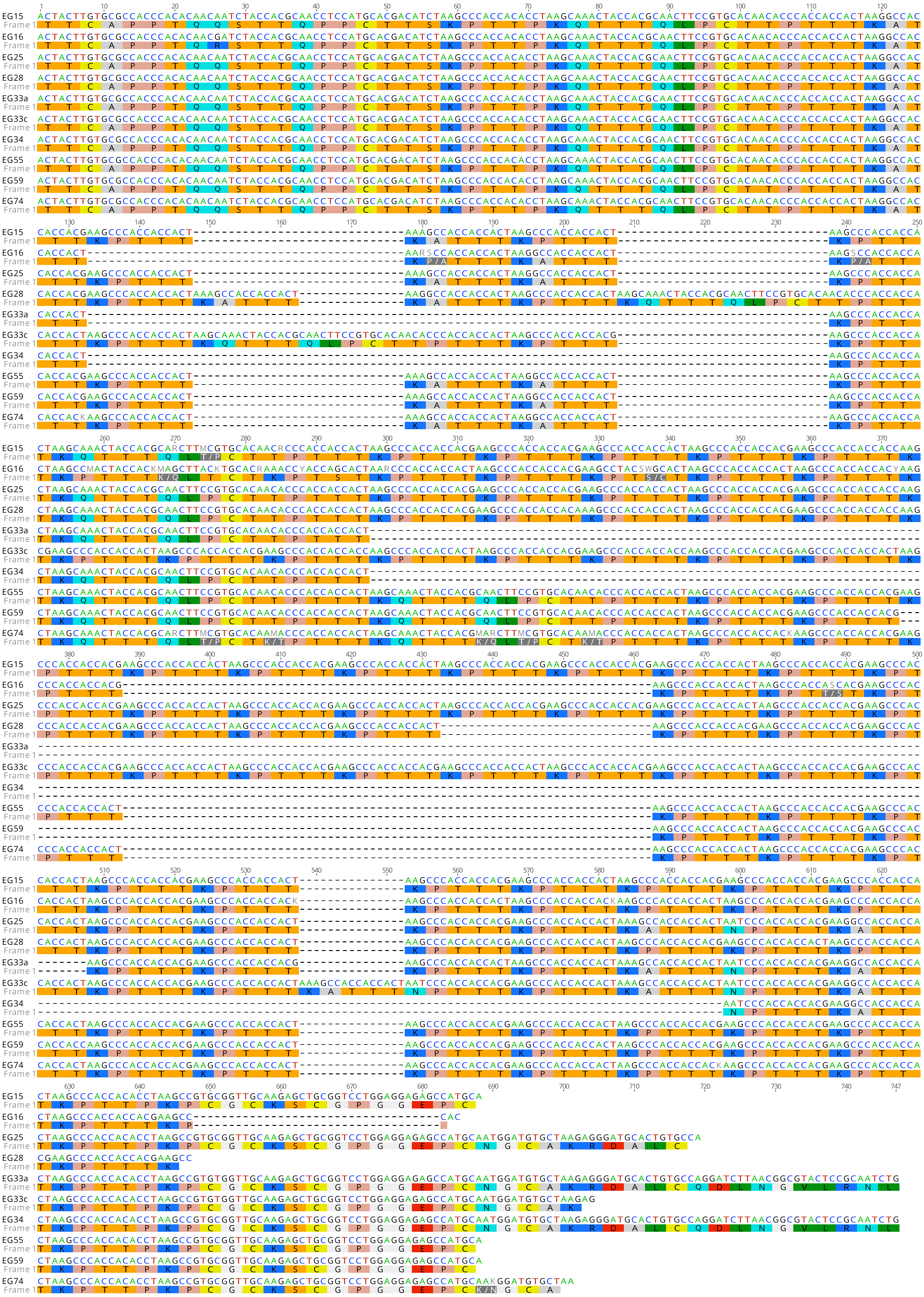
Chavroche-sgs3
Chavroche2-sgs3
Chavroche3-sgs3
Cotonou-sgs3
Dehli1-sgs3
Delhi2-sgs3
Dehli B-sgs3
Gally A sgs3
Gally B sgs3
Gally C sgs3
Gally D sgs3
EFB_sgs3
EF3-sgs3
Frame 1


EG15
EG16
EG25
EG28
EG33a
EG33c
EG34
EG55
EG59
EG74
Frame 1
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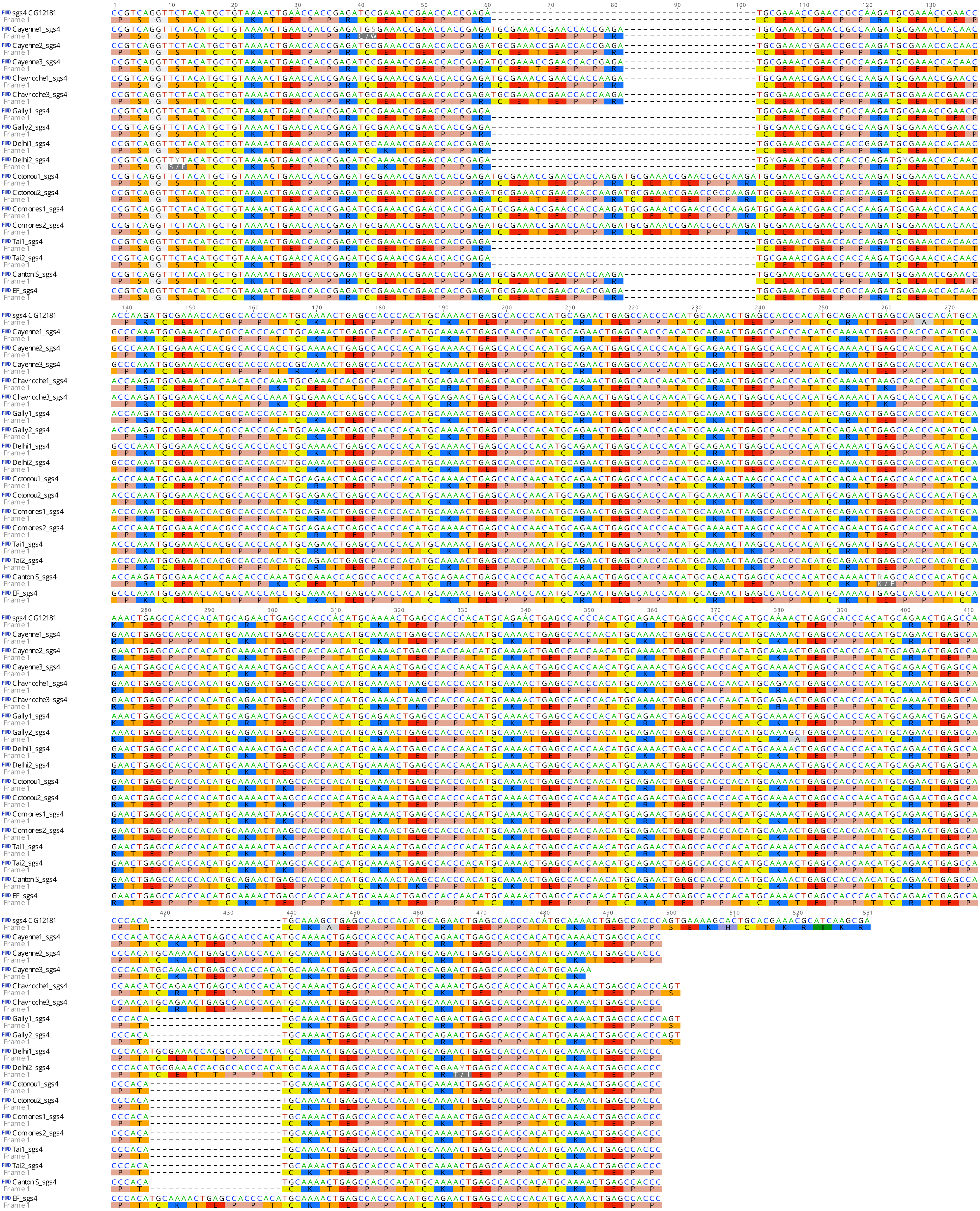sgs4 CG12181
Cayenne1_sgs4
Cayenne2_sgs4
Cayenne3_sgs4
Chavroche1_sgs4
Chavroche3_sgs4
Gally1_sgs4
Gally2_sgs4
Delhi1_sgs4
Delhi2_sgs4
Cotonou1_sgs4
Cotonou2_sgs4
Comores1_sgs4
Comores2_sgs4
Tai1_sgs4
Tai2_sgs4
Canton S_sgs4
EF_sgs4
Frame 1
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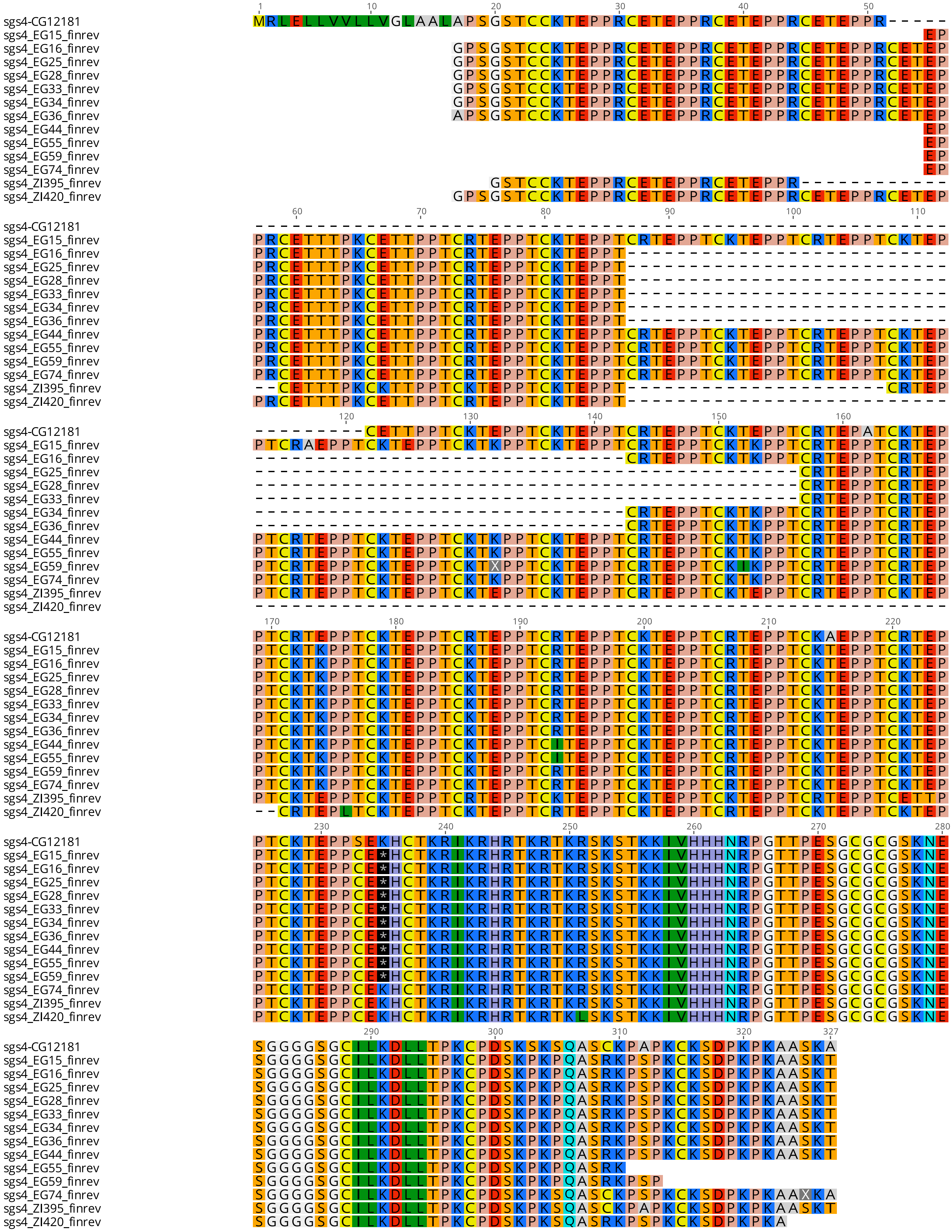

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sgs4_EG15_finrev                                                          EP
sgs4_EG16_finrev                    GPSGSTCCKTEPPRCETEPPRCETEPPRCETEPPRCETEP
sgs4_EG25_finrev                    GPSGSTCCKTEPPRCETEPPRCETEPPRCETEPPRCETEP
sgs4_EG28_finrev                    GPSGSTCCKTEPPRCETEPPRCETEPPRCETEPPRCETEP
sgs4_EG33_finrev                    GPSGSTCCKTEPPRCETEPPRCETEPPRCETEPPRCETEP
sgs4_EG34_finrev                    GPSGSTCCKTEPPRCETEPPRCETEPPRCETEPPRCETEP
sgs4_EG36_finrev                    APSGSTCCKTEPPRCETEPPRCETEPPRCETEPPRCETEP
sgs4_EG44_finrev                                                          EP
sgs4_EG55_finrev                                                          EP
sgs4_EG59_finrev                                                          EP
sgs4_EG74_finrev                                                          EP
sgs4_ZI395_finrev                      GSTCCKTEPPRCETEPPRCETEPPR------------
sgs4_ZI420_finrev                   GPSGSTCCKTEPPRCETEPPRCETEPPRCETEPPRCETEP

                     60        70        80        90        100       110
sgs4-CG12181      --------------------------------------------------------
sgs4_EG15_finrev  PRCETTTPKCETTPPTCRTEPPTCKTEPPTCRTEPPTCKTEPPTCRTEPPTCKTEP
sgs4_EG16_finrev  PRCETTTPKCETTPPTCRTEPPTCKTEPPT--------------------------
sgs4_EG25_finrev  PRCETTTPKCETTPPTCRTEPPTCKTEPPT--------------------------
sgs4_EG28_finrev  PRCETTTPKCETTPPTCRTEPPTCKTEPPT--------------------------
sgs4_EG33_finrev  PRCETTTPKCETTPPTCRTEPPTCKTEPPT--------------------------
sgs4_EG34_finrev  PRCETTTPKCETTPPTCRTEPPTCKTEPPT--------------------------
sgs4_EG36_finrev  PRCETTTPKCETTPPTCRTEPPTCKTEPPT--------------------------
sgs4_EG44_finrev  PRCETTTPKCETTPPTCRTEPPTCKTEPPTCRTEPPTCKTEPPTCRTEPPTCKTEP
sgs4_EG55_finrev  PRCETTTPKCETTPPTCRTEPPTCKTEPPTCRTEPPTCKTEPPTCRTEPPTCKTEP
sgs4_EG59_finrev  PRCETTTPKCETTPPTCRTEPPTCKTEPPTCRTEPPTCKTEPPTCRTEPPTCKTEP
sgs4_EG74_finrev  PRCETTTPKCETTPPTCRTEPPTCKTEPPTCRTEPPTCKTEPPTCRTEPPTCKTEP
sgs4_ZI395_finrev --CETTTPKCKTTPPTCKTEPPTCKTEPPT---------------------CRTEP
sgs4_ZI420_finrev PRCETTTPKCETTPPTCRTEPPTCKTEPPT--------------------------

                         120       130       140       150       160
sgs4-CG12181      ---------CETTPPTCKTEPPTCKTEPPTCRTEPPTCKTEPPTCRTEPATCKTEP
sgs4_EG15_finrev  PTCRAEPPTCKTEPPTCKTKPPTCKTEPPTCRTEPPTCKTKPPTCRTEPPTCRTEP
sgs4_EG16_finrev  ------------------------------CRTEPPTCKTKPPTCRTEPPTCRTEP
sgs4_EG25_finrev  --------------------------------------------CRTEPPTCRTEP
sgs4_EG28_finrev  --------------------------------------------CRTEPPTCRTEP
sgs4_EG33_finrev  --------------------------------------------CRTEPPTCRTEP
sgs4_EG34_finrev  ------------------------------CRTEPPTCKTKPPTCRTEPPTCRTEP
sgs4_EG36_finrev  ------------------------------CRTEPPTCKTKPPTCRTEPPTCRTEP
sgs4_EG44_finrev  PTCRTEPPTCKTEPPTCKTKPPTCKTEPPTCRTEPPTCKTKPPTCRTEPPTCRTEP
sgs4_EG55_finrev  PTCRTEPPTCKTEPPTCKTKPPTCKTEPPTCRTEPPTCKTKPPTCRTEPPTCRTEP
sgs4_EG59_finrev  PTCRTEPPTCKTEPPTCKTXPPTCKTEPPTCRTEPPTCKIKPPTCRTEPPTCRTEP
sgs4_EG74_finrev  PTCRTEPPTCKTEPPTCKTKPPTCKTEPPTCRTEPPTCKTKPPTCRTEPPTCRTEP
sgs4_ZI395_finrev PTCRTEPPTCKTEPPTCKTEPPTCKTEPPTCRTEPPTCKTEPPTCRTEPPTCKTEP
sgs4_ZI420_finrev --------------------------------------------------------

                   170       180       190       200       210       220
sgs4-CG12181      PTCRTEPPTCKTEPPTCRTEPPTCRTEPPTCKTEPPTCRTEPPTCKAEPPTCRTEP
sgs4_EG15_finrev  PTCKTKPPTCKTEPPTCKTEPPTCRTEPPTCKTEPPTCRTEPPTCKTEPPTCKTEP
sgs4_EG16_finrev  PTCKTKPPTCKTEPPTCKTEPPTCRTEPPTCKTEPPTCRTEPPTCKTEPPTCKTEP
sgs4_EG25_finrev  PTCKTKPPTCKTEPPTCKTEPPTCRTEPPTCKTEPPTCRTEPPTCKTEPPTCKTEP
sgs4_EG28_finrev  PTCKTKPPTCKTEPPTCKTEPPTCRTEPPTCKTEPPTCRTEPPTCKTEPPTCKTEP
sgs4_EG33_finrev  PTCKTKPPTCKTEPPTCKTEPPTCRTEPPTCKTEPPTCRTEPPTCKTEPPTCKTEP
sgs4_EG34_finrev  PTCKTKPPTCKTEPPTCKTEPPTCRTEPPTCKTEPPTCRTEPPTCKTEPPTCKTEP
sgs4_EG36_finrev  PTCKTKPPTCKTEPPTCKTEPPTCRTEPPTCKTEPPTCRTEPPTCKTEPPTCKTEP
sgs4_EG44_finrev  PTCKTKPPTCKTEPPTCKTEPPTCITEPPTCKTEPPTCRTEPPTCKTEPPTCKTEP
sgs4_EG55_finrev  PTCKTKPPTCKTEPPTCKTEPPTCITEPPTCKTEPPTCRTEPPTCKTEPPTCKTEP
sgs4_EG59_finrev  PTCKTKPPTCKTEPPTCKTEPPTCRTEPPTCKTEPPTCRTEPPTCKTEPPTCKTEP
sgs4_EG74_finrev  PTCKTKPPTCKTEPPTCKTEPPTCRTEPPTCKTEPPTCRTEPPTCKTEPPTCKTEP
sgs4_ZI395_finrev PTCKTEPPTCKTEPPTCRTEPPTCKTEPPTCKTEPPTCKTEPPTCRTEPPTCETTP
sgs4_ZI420_finrev --CRTEPLTCKTEPPTCKTEPPTCRTEPPTCKTEPPTCRTEPPTCKTEPPTCKTEP

                       230       240       250       260       270       280
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sgs4_EG15_finrev  PTCKTEPPCE*HCTKRIKRHRTKRTKRSKSTKKIVHHHNRPGTTPESGCGCGSKNE
sgs4_EG16_finrev  PTCKTEPPCE*HCTKRIKRHRTKRTKRSKSTKKIVHHHNRPGTTPESGCGCGSKNE
sgs4_EG25_finrev  PTCKTEPPCE*HCTKRIKRHRTKRTKRSKSTKKIVHHHNRPGTTPESGCGCGSKNE
sgs4_EG28_finrev  PTCKTEPPCE*HCTKRIKRHRTKRTKRSKSTKKIVHHHNRPGTTPESGCGCGSKNE
sgs4_EG33_finrev  PTCKTEPPCE*HCTKRIKRHRTKRTKRSKSTKKIVHHHNRPGTTPESGCGCGSKNE
sgs4_EG34_finrev  PTCKTEPPCE*HCTKRIKRHRTKRTKRSKSTKKIVHHHNRPGTTPESGCGCGSKNE
sgs4_EG36_finrev  PTCKTEPPCE*HCTKRIKRHRTKRTKRSKSTKKIVHHHNRPGTTPESGCGCGSKNE
sgs4_EG44_finrev  PTCKTEPPCE*HCTKRIKRHRTKRTKRSKSTKKIVHHHNRPGTTPESGCGCGSKNE
sgs4_EG55_finrev  PTCKTEPPCE*HCTKRIKRHRTKRTKRSKSTKKIVHHHNRPGTTPESGCGCGSKNE
sgs4_EG59_finrev  PTCKTEPPCE*HCTKRIKRHRTKRTKRSKSTKKIVHHHNRPGTTPESGCGCGSKNE
sgs4_EG74_finrev  PTCKTEPPCEKHCTKRIKRHRTKRTKRSKSTKKIVHHHNRPGTTPESGCGCGSKNE
sgs4_ZI395_finrev PTCKTEPPCEKHCTKRIKRHRTKRTKRSKSTKKIVHHHNRPGTTPESGCGCGSKNE
sgs4_ZI420_finrev PTCKTEPPCEKHCTKRIKRHRTKRTKLSKSTKKIVHHHNRPGTTPESGCGCGSKNE

                           290       300       310       320    327
sgs4-CG12181      SGGGGSGCILKDLLTPKCPDSKSKSQASCKPAPKCKSDPKPKAASKA
sgs4_EG15_finrev  SGGGGSGCILKDLLTPKCPDSKPKPQASRKPSPKCKSDPKPKAASKT
sgs4_EG16_finrev  SGGGGSGCILKDLLTPKCPDSKPKPQASRKPSPKCKSDPKPKAASKT
sgs4_EG25_finrev  SGGGGSGCILKDLLTPKCPDSKPKPQASRKPSPKCKSDPKPKAASKT
sgs4_EG28_finrev  SGGGGSGCILKDLLTPKCPDSKPKPQASRKPSPKCKSDPKPKAASKT
sgs4_EG33_finrev  SGGGGSGCILKDLLTPKCPDSKPKPQASRKPSPKCKSDPKPKAASKT
sgs4_EG34_finrev  SGGGGSGCILKDLLTPKCPDSKPKPQASRKPSPKCKSDPKPKAASKT
sgs4_EG36_finrev  SGGGGSGCILKDLLTPKCPDSKPKPQASRKPSPKCKSDPKPKAASKT
sgs4_EG44_finrev  SGGGGSGCILKDLLTPKCPDSKPKPQASRKPSPKCKSDPKPKAASKT
sgs4_EG55_finrev  SGGGGSGCILKDLLTPKCPDSKPKPQASRK
sgs4_EG59_finrev  SGGGGSGCILKDLLTPKCPDSKPKPQASRKPSP
sgs4_EG74_finrev  SGGGGSGCILKDLLTPKCPDSKPKSQASCKPSPKCKSDPKPKAAXKA
sgs4_ZI395_finrev SGGGGSGCILKDLLTPKCPDSKPKSQASCKPAPKCKSDPKPKAASKT
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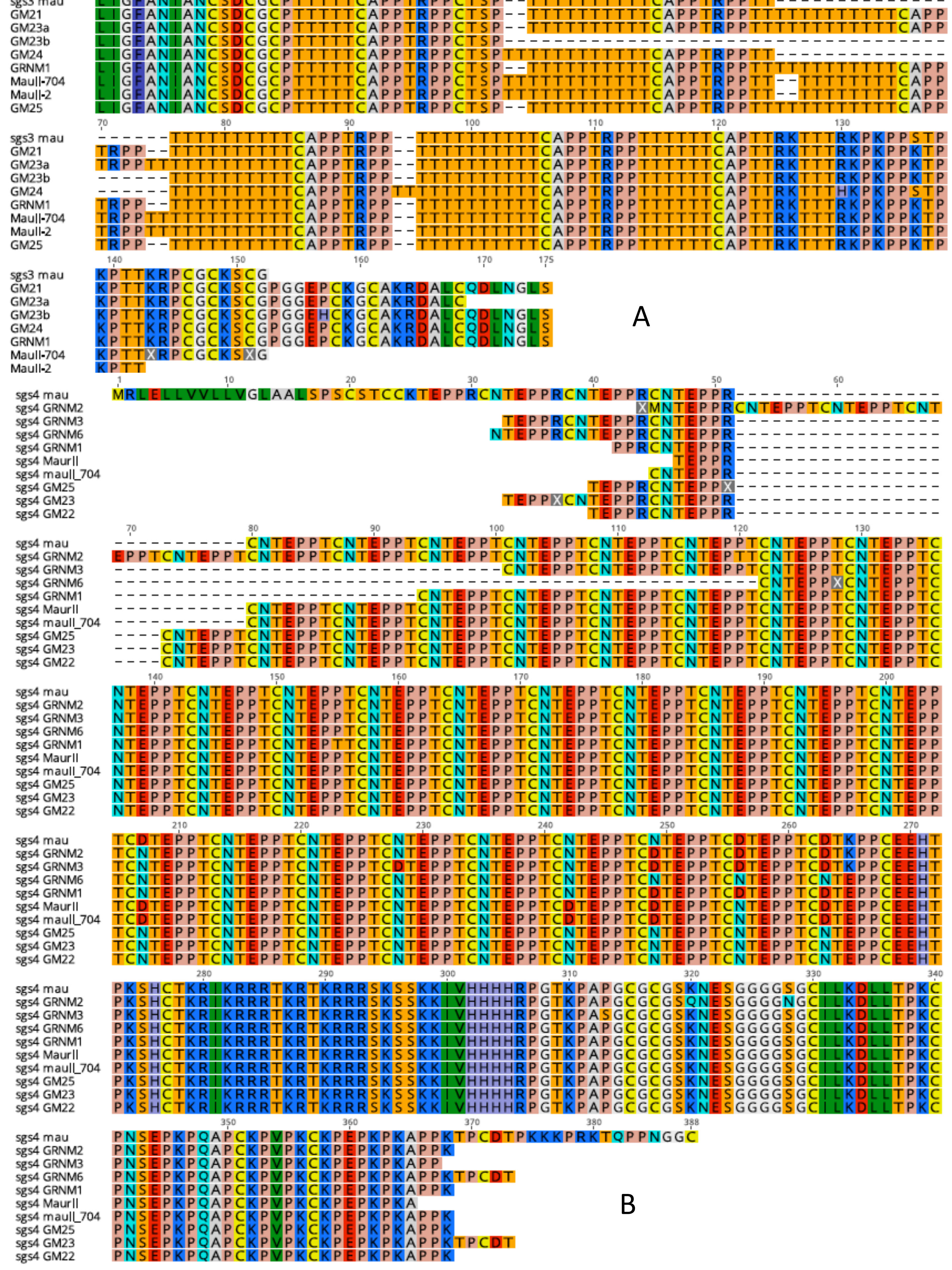

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GM23a           LIGFANIANCSDCGCPTTTTTCAPPTRPPCTSP--TTTTTTTTTTCAPPTRPPTTTTTTTTTTTTCAPP
GM23b           LIGFANIANCSDCGCPTTTTTCAPPTRPPCTSP------------------------------------
GM24            LIGFANIANCSDCGCPTTTTTCAPPTRPPCTSPTTTTTTTTTTTTCAPPTRPPTT--------------
GRNM1           LIGFANIANCSDCGCPTTTTTCAPPTRPPCTSP--TTTTTTTTTTCAPPTRPPTTTTTTTTTTTTCAPP
MauII-704       LIGFANIANCSDCGCPTTTTTCAPPTRPPCTSPTTTTTTTTTTTTCAPPTRPPTT--TTTTTTTTCAPP
MauII-2         LIGFANIANCSDCGCPTTTTTCAPPTRPPCTSPTTTTTTTTTTTTCAPPTRPPTT--TTTTTTTTCAPP
GM25            LIGFANIANCSDCGCPTTTTTCAPPTRPPCTSP--TTTTTTTTTTCAPPTRPPTTTTTTTTTTTTCAPP

                70        80        90        100       110       120       130
sgs3 mau        ------TTTTTTTTTTCAPPTRPP--TTTTTTTTTTCAPPTRPPTTTTTTCAPTTRKTTTRKPKPPSTP
GM21            TRPP--TTTTTTTTTTCAPPTRPP--TTTTTTTTTTCAPPTRPPTTTTTTCAPTTRKTTTRKPKPPKTP
GM23a           TRPPTTTTTTTTTTTTCAPPTRPP--TTTTTTTTTTCAPPTRPPTTTTTTCAPTTRKTTTRKPKPPKTP
GM23b           ------TTTTTTTTTTCAPPTRPP--TTTTTTTTTTCAPPTRPPTTTTTTCAPTTRKTTTRKPKPPKTP
GM24            ------TTTTTTTTTTCAPPTRPPTTTTTTTTTTTTCAPPTRPPTTTTTTCAPTTRKTTTHKPKPPSTP
GRNM1           TRPP--TTTTTTTTTTCAPPTRPP--TTTTTTTTTTCAPPTRPPTTTTTTCAPTTRKTTTRKPKPPKTP
MauII-704       TRPPTTTTTTTTTTTTCAPPTRPP--TTTTTTTTTTCAPPTRPPTTTTTTCAPTTRKTTTRKPKPPKTP
MauII-2         TRPPTTTTTTTTTTTTCAPPTRPP--TTTTTTTTTTCAPPTRPPTTTTTTCAPTTRKTTTRKPKPPKTP
GM25            TRPP--TTTTTTTTTTCAPPTRPP--TTTTTTTTTTCAPPTRPPTTTTTTCAPTTRKTTTRKPKPPKTP

                 140       150       160       170  175
sgs3 mau        KPTTKRPCGCKSCG
GM21            KPTTKRPCGCKSCGPGGEPCKGCAKRDALCQDLNGLS
GM23a           KPTTKRPCGCKSCGPGGEPCKGCAKRDALC
GM23b           KPTTKRPCGCKSCGPGGEHCKGCAKRDALCQDLNGLS
GM24            KPTTKRPCGCKSCGPGGEPCKGCAKRDALCQDLNGLS
GRNM1           KPTTKRPCGCKSCGPGGEPCKGCAKRDALCQDLNGLS
MauII-704       KPTTXRPCGCKSXG
MauII-2         KPTT
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                1        10        20        30        40        50        60
sgs4 mau        MRLELLVVLLVGLAALSPSCSTCCKTEPPRCNTEPPRCNTEPPRCNTEPPR-----------------
sgs4 GRNM2                                                 XMNTEPPRCNTEPPTCNTEPPTCNT
sgs4 GRNM3                                      TEPPRCNTEPPRCNTEPPR-----------------
sgs4 GRNM6                                     NTEPPRCNTEPPRCNTEPPR-----------------
sgs4 GRNM1                                               PPRCNTEPPR-----------------
sgs4 MaurII                                                   TEPPR-----------------
sgs4 mauII_704                                              CNTEPPR-----------------
sgs4 GM25                                              TEPPRCNTEPPX-----------------
sgs4 GM23                                       TEPPXCNTEPPRCNTEPPR-----------------
sgs4 GM22                                              TEPPRCNTEPPR-----------------

                 70        80        90        100       110       120       130
sgs4 mau        -----------CNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTC
sgs4 GRNM2      EPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPTTCNTEPPTCNTEPPTC
sgs4 GRNM3      --------------------------------CNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTC
sgs4 GRNM6      -----------------------------------------------------CNTEPPXCNTEPPTC
sgs4 GRNM1      -------------------------CNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTC
sgs4 MaurII     -----------CNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTC
sgs4 mauII_704  -----------CNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTC
sgs4 GM25       ----CNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTC
sgs4 GM23       ----CNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTC
sgs4 GM22       ----CNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTC

                   140       150       160       170       180       190       200
sgs4 mau        NTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPP
sgs4 GRNM2      NTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPP
sgs4 GRNM3      NTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPP
sgs4 GRNM6      NTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPP
sgs4 GRNM1      NTEPPTCNTEPPTCNTEPTTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPP
sgs4 MaurII     NTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPP
sgs4 mauII_704  NTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPP
sgs4 GM25       NTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPP
sgs4 GM23       NTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPP
sgs4 GM22       NTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPP

                     210       220       230       240       250       260       270
sgs4 mau        TCDTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCDTEPPTCDTKPPCEEHT
sgs4 GRNM2      TCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCDTEPPTCDTEPPTCDTKPPCEEHT
sgs4 GRNM3      TCNTEPPTCNTEPPTCNTEPPTCDTEPPTCNTEPPTCNTEPPTCDTEPPTCDTEPPTCDTKPPCEEHT
sgs4 GRNM6      TCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPCEEHT
sgs4 GRNM1      TCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCDTEPPTCDTEPPTCDTEPPCEEHT
sgs4 MaurII     TCDTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCDTEPPTCDTEPPTCNTEPPTCDTEPPCEEHT
sgs4 mauII_704  TCDTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCDTEPPTCDTEPPTCNTEPPTCDTEPPCEEHT
sgs4 GM25       TCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPCEEHT
sgs4 GM23       TCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPCEEHT
sgs4 GM22       TCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPTCNTEPPCEEHT

                       280       290       300       310       320       330       340
sgs4 mau        PKSHCTKRIKRRRTKRTKRRRSKSSKKIVHHHHRPGTKPAPGCGCGSKNESGGGGSGCILKDLLTPKC
sgs4 GRNM2      PKSHCTKRIKRRRTKRTKRRRSKSSKKIVHHHHRPGTKPAPGCGCGSQNESGGGGNGCILKDLLTPKC
sgs4 GRNM3      PKSHCTKRIKRRRTKRTKRRRSKSSKKIVHHHHRPGTKPASGCGCGSKNESGGGGSGCILKDLLTPKC
sgs4 GRNM6      PKSHCTKRIKRRRTKRTKRRRSKSSKKIVHHHHRPGTKPAPGCGCGSKNESGGGGSGCILKDLLTPKC
sgs4 GRNM1      PKSHCTKRIKRRRTKRTKRRRSKSSKKIVHHHHRPGTKPAPGCGCGSKNESGGGGSGCILKDLLTPKC
sgs4 MaurII     PKSHCTKRIKRRRTKRTKRRRSKSSKKIVHHHHRPGTKPAPGCGCGSKNESGGGGSGCILKDLLTPKC
sgs4 mauII_704  PKSHCTKRIKRRRTKRTKRRRSKSSKKIVHHHHRPGTKPAPGCGCGSKNESGGGGSGCILKDLLTPKC
sgs4 GM25       PKSHCTKRIKRRRTKRTKRRRSKSSKKIVHHHHRPGTKPAPGCGCGSKNESGGGGSGCILKDLLTPKC
sgs4 GM23       PKSHCTKRIKRRRTKRTKRRRSKSSKKIVHHHHRPGTKPAPGCGCGSKNESGGGGSGCILKDLLTPKC
sgs4 GM22       PKSHCTKRIKRRRTKRTKRRRSKSSKKIVHHHHRPGTKPAPGCGCGSKNESGGGGSGCILKDLLTPKC

                         350       360       370       380     388
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sgs4 GRNM2      PNSEPKPQAPCKPVPKCKPEPKPKAPPK
sgs4 GRNM3      PNSEPKPQAPCKPVPKCKPEPKPKAPP
sgs4 GRNM6      PNSEPKPQAPCKPVPKCKPEPKPKAPPKTPCDT
sgs4 GRNM1      PNSEPKPQAPCKPVPKCKPEPKPKAPPK
sgs4 MaurII     PNSEPKPQAPCKPVPKCKPEPKPKA
sgs4 mauII_704  PNSEPKPQAPCKPVPKCKPEPKPKAPPK
sgs4 GM25       PNSEPKPQAPCKPVPKCKPEPKPKAPPK
sgs4 GM23       PNSEPKPQAPCKPVPKCKPEPKPKAPPKTPCDT
sgs4 GM22       PNSEPKPQAPCKPVPKCKPEPKPKAPPK
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	Sgs1	Sgs3-7-8 family	Sgs1-3-7-8 family	Sgs4	Sgs5-5bis family
D. melanogaster	1	3	4	1	2
D. simulans	1	3	4	1	2
D. sechellia	1	3	4	1	2
D. mauritiana	1	2	3	1	1
D. santomea	1	4	5	1	2
D. yakuba	1	4	5	1	2
D. erecta	0	3	3	1	1
D. eugracilis	1	4	5	0	2
D. takahashi	1	3	4	0	2
D. suzukii	1	5	6	0	2
D. biarmipes	1	4	5	0	2
D. elegans	1	3	4	0	1
D. rhopaloa	1	4	5	0	1
D. ficusphila	1	3	4	0	2
D. kikkawai	0	2	2	0	2
D. ananassae	0	2	2	0	2
D. bipectinata	0	4	4	0	2
D. pseudoobscura	0	3	3	0	1
D. willistoni	0	4	4	0	0
D. virilis	0	2	2	0	1
Lambda value	0,0036503	0,003650259	0,003650259	0,0036503	0,003650259
P-value	0,2925	0,013	0,005	0,5795	0,107
Tree used	(((drho:11.1	(((drho:11.134	(((drho:11.1347,	((dere:5.733	(((drho:11.1347

```
7,dele:11.1347):5.86695,(((dsuz:6.86108,dbia:6.86108):4.95065,dtak:11.8117):3.4
```

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2837,(((dere:5.73328,(dyak:1.0,dsan:1.0):4.73328):1.52117,(((dsec:1.35937,dsim:1.35937):
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:1.0,dmau:2.35937):1.16816,dmel:3.52753):3.72691):7.01828,deug:14.24007):1.0):1.7615)
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:1.39134,dfic:18.3929):9.20704;
```

Table S2 : List of primers used for this study. Different combinations were used to amplify glue genes. All primers were chosen outside the repeated regions. *D. sechellia*, *D. santomea*, *D. virilis* and *D. biarmipes* were resequenced because of uncertainties or putative errors in the online sequences. *D. melanogaster* and *D. mauritiana* were resequenced for studying RNV in *Sgs3* and *Sgs4*, or confirming the presence of premature stop codons in *Sgs4* and *Sgs5* of *D. melanogaster*.

Sgs1

species	Forward primers	Reverse primers
D. melanogaster	ATGAAAGTCGCCCTTATCTT	TGTCAGTGTCACAGGGTTGC
D. sechellia	TCGTCCTTGTCCTTGCCATC	TTACGTTCGTGTGCACAAGCA

Sgs3

species	Forward primers	Reverse primers
D. melanogaster	TCCGCTAATGTTGCCAACTG TAATGTTGCCAACTGTTGC CATGAAGCTGACCATTGCTA	CATCCATTGCATGGCTCTCC ATTGACGGATCTTGCGCTC GACGCATTGACGGATCTTGC
D. sechellia	GCTGACCATTGCTACCATTG	CTTAGCGCATCCTGTGCAAG
D. santomea	GAAGCTGACCATTGCCATCGC GTGCACAGTCCCTGCCTCTT	TAAGATCCGTGCACAGTCCC
D. mauritiana	ATCCTGCTTATTGGCTTCGC	AAGCCGTTGAGATCCTGGCA
D. virilis	TGCTCGGCTGAATGCGAGTG	CAAGAGCTCCTTGCAGAGCG GGTCCTTGTGGTGGACACGC
D. biarmipes	AGCCCATGTGAAGTGGAGTC GGATGCACCACCGGGACTGA ACCGGGACTGAATGTGGTTG TGGAGTCTCCACCCTGTGA	GGGCTCTCCGCAGACGCATTG CATTGCCGGATCTTGCGTTC ACAAACGCACTGGCGGATTC TCCAGACCTCGGACTGTGTTG

Sgs4

species	Forward primers	Reverse primers
D. melanogaster	CACTTGCCCCGTCAGGTTCTAC TGTCTATGTCTAACCATCGC	TACAGCATGTAGAACCTGAC GCGGTTTCTTGGTGGTGTTC TGTCGCTTGATGCGTTTCGT
D. sechellia	GGTCTGGCTGCACTTTCGCC	TACAGCATGTAGAACCTGAC
D. santomea	TTATTGGTCGGGTTGGCTG TCGGGTTGGCTGCACTTAC	GGTGGTGGCACATGGTTTCG CACATGGTTTCGGCTGCGA
D. mauritiana	CTGCACTTTCGCCGTCATGT	CTGGGTCTTCCGTGGTTTC

Sgs5

species	Forward primers	Reverse primers
D. melanogaster	CATGGACAAGCCGTCCAGGA	GTAACGTGATCCAACTGAATCC

Table S3: Assembly/Annotation error estimation and gene gain/loss rates in a single λ model in the 25 *Drosophlia* species included in this study compared to previous studies using fewer species.

	$\boldsymbol{\lambda}$ (No Error Model)	$\boldsymbol{\varepsilon}$ (Estimated error)	$\boldsymbol{\lambda}$ (Error Model = $\boldsymbol{\varepsilon}$)
25 *Drosophila* species in this study	0.00365	0.04434	0.00340
12 *Drosophila* species (Han et al. 2013)	0.00121	0.04102	0.00059
12 *Drosophila* species (Hahn et al. 2007)	0.00121	NA	NA

Table S4: Summary of gene gain and loss events inferred after correcting for annotation and assembly error across all 25 *Drosophila* species. The number of rapidly evolving families is shown in parentheses for each type of change.

Species	Expansions			Contractions			No Change	Avg. Expansion
	Families	Genes gained	genes/ expansion	Families	Genes lost	genes/ contraction		
pseudoobscura	307 (55)	390	1.27	325 (79)	356	1.1	8747	0.003625
miranda	161 (14)	189	1.17	377 (27)	428	1.14	8841	-0.025482
bipectinata	425 (43)	579	1.36	167 (12)	206	1.23	8787	0.039770
eugracilis	461 (34)	649	1.41	271 (6)	311	1.15	8647	0.036038
busckii	844 (23)	1288	1.53	712 (5)	801	1.13	7823	0.051925
takahashii	477 (60)	874	1.83	139 (4)	148	1.06	8763	0.077407
erecta	102 (20)	132	1.29	198 (25)	286	1.44	9079	-0.016420
sechellia	1184 (233)	2020	1.71	443 (83)	480	1.08	7752	0.164197
persimilis	1243 (254)	1979	1.59	458 (66)	493	1.08	7678	0.158439
kikkawai	558 (30)	811	1.45	362 (4)	410	1.13	8459	0.042755
arizonae	154 (31)	163	1.06	531 (106)	578	1.09	8694	-0.044248
virilis	329 (21)	541	1.64	288 (1)	303	1.05	8762	0.025376
elegans	347 (24)	464	1.34	259 (24)	357	1.38	8773	0.011408
suzukii	1472 (105)	2108	1.43	219 (8)	238	1.09	7688	0.199382
simulans	151 (35)	192	1.27	168 (66)	260	1.55	9060	-0.007250
yakuba	673 (84)	891	1.32	120 (6)	145	1.21	8586	0.079539
melanogaster	60 (13)	88	1.47	166 (13)	196	1.18	9153	-0.011515
mojavensis	320 (101)	470	1.47	166 (47)	179	1.08	8893	0.031027
grimshawi	843 (25)	1218	1.44	633 (2)	683	1.08	7903	0.057042
willistoni	603 (13)	895	1.48	649 (1)	713	1.1	8127	0.019405
navojoa	202 (25)	227	1.12	1934 (74)	2200	1.14	7243	-0.210364
rhopaloa	1127 (96)	1753	1.56	153 (2)	159	1.04	8099	0.169954
biarmipes	150 (9)	184	1.23	230 (21)	288	1.25	8999	-0.011089
ananassae	270 (28)	464	1.72	237 (13)	278	1.17	8872	0.019832
ficusphila	514 (29)	685	1.33	341 (7)	393	1.15	8524	0.031133